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OM protein - protein search, using sw model

Run on: May 7, 2002, 11:58:52 ; Search time 26.38 seconds
(without alignments)
190.229 Million cell updates/sec

Title: US-09-772-103-2
Perfect score: 1174
Sequence: 1 MACLGFORHKAQLNLRWTW.....MPPEPECEKQFQYFPIPN 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

al number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1158	98.6	233	3	US-08-228-208A-17
2	1103.5	94.0	234	1	US-08-505-058-1
3	1103.5	94.0	234	1	US-08-459-818-21
4	1103.5	94.0	234	2	US-08-889-666-21
5	1103.5	94.0	234	2	US-08-465-078-21
6	1103.5	94.0	234	2	US-08-725-776-21
7	1103.5	94.0	234	2	US-08-488-062-21
8	970	82.6	187	1	US-08-067-684-14
9	970	82.6	187	1	US-08-008-898-14
10	970	82.6	187	2	US-08-459-818-14
11	970	82.6	187	2	US-08-889-666-14
12	970	82.6	187	2	US-08-465-078-14
13	970	82.6	187	2	US-08-725-776-14
14	970	82.6	187	3	US-08-488-062-14
15	970	82.6	187	3	US-08-228-208A-14
16	857	82.4	187	5	PCT-US95-06726-36
17	857	73.0	223	3	US-08-228-208A-18
18	804.5	68.5	234	1	US-08-505-058-2
19	804.5	68.5	234	2	US-08-459-818-22
20	804.5	68.5	234	2	US-08-889-666-22
21	804.5	68.5	234	2	US-08-465-078-22
22	804.5	68.5	234	2	US-08-725-776-22
23	804.5	68.5	234	2	US-08-488-062-22
24	648	55.2	124	3	US-08-630-172-4
25	648	55.2	124	4	US-09-375-419-4
26	648	55.2	357	3	US-08-630-172-20
27	648	55.2	357	4	US-09-375-419-20

ALIGNMENTS

RESULT 1
US-08-228-208A-17
; Sequence 17, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Wallace, Philip M.
; TITLE OF INVENTION: CTLA4/CD281g HYBRID FUSION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-228-208A-17

Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl

28 638.5 54.4 253 2 US-08-459-818-20
29 638.5 54.4 253 2 US-08-889-666-20
30 638.5 54.4 253 2 US-08-465-078-20
31 638.5 54.4 253 2 US-08-725-776-20
32 638.5 54.4 253 2 US-08-488-062-20
33 638.5 54.4 502 2 US-08-459-818-19
34 638.5 54.4 502 2 US-08-889-666-19
35 638.5 54.4 502 2 US-08-465-078-19
36 638.5 54.4 502 2 US-08-725-776-19
37 638.5 54.4 502 2 US-08-488-062-19
38 592 50.4 137 3 US-08-804-180C-2
39 534 45.5 174 3 US-08-505-058-6
40 222.5 19.0 226 1 US-08-459-818-26
41 222.5 19.0 226 2 US-08-889-666-26
42 222.5 19.0 226 2 US-08-465-078-26
43 222.5 19.0 226 2 US-08-725-776-26
44 222.5 19.0 226 2 US-08-488-062-26
45 222.5 19.0 226 2

QY 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCCKAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCCKAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDS--ICTGTSSGNQVNLTIQ 118
Db 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMTGNELTFLDSDSXXICTGTSSGNQVNLTIQ 120
QY 119 LRAMDTGLYICKVELMYPYPYL-GIGNGAQIYVIDPEPC-----PDSDFLLWILAIVSS 172
Db 121 LRAMDTGLYICKVELMYPYPYLXGIGNGTQIYVIDPEPCXXXPDSDFLWILAIVSS 180
QY 173 GLFFYSFLLT-AVSLSKMLKKRSLPTGTVVYKMPPTPECE--KQFQYRIPIN 223
Db 181 GLFFYSFLLTAVSLSKMLKKRSLPTGTVVYKMPPTPECEXXKQFQYRIPIN 234

RESULT 3
US-08-459-818-21
; Sequence 21, Application US/08459818
; Patent No. 5851795
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,818
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.35US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-818-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 1.4e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCCKAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCCKAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDSICTGTSSGNQVNLTIQGLR 120
Db 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDSICTGTSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMYPYPYLXGIGNGTQIYVIDPEPCPSDSDFLWILAIVSSGLFFYSFL 180
Db 121 AMDTGLYICKVELMYPYPYLXGIGNGTQIYVIDPEPCPSDSDFLWILAIVSSGLFFYSFL 180
QY 181 LTAVSLSKMLKKRSLPTGTVVYKMPPTPECEKQFQYRIPIN 223
Db 181 LTAVSLSKMLKKRSLPTGTVVYKMPPTPECEKQFQYRIPIN 223

RESULT 2
US-08-505-058-1
; Sequence 1, Application US/08505058
; Patent No. 5773253
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Peach, Robert
; TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,058
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/228,208
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.3005I1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-505-058-1

Query Match 94.0%; Score 1103.5; DB 1; Length 234;
Best Local Similarity 94.0%; Pred. No. 1.4e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 119 LRAMDTGLYICKVELMPPPPYL-GINGAQIYVIDPEPC-----PDSDFLLWILAASS 172
 Db 121 LRAMDTGLYICKVELMPPPPYLXGIGNGTQIYVIDPEPCXXXXPDSDFLLWILAASS 180
 QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTTGVYVKMPPTPECE--KQFPYFIPIN 223
 Db 181 GLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKMPPTPECEXXXKQFPYFIPIN 234

RESULT 4

US-08-889-666-21
 ; Sequence 21, Application US/08889666
 ; Patent No. 5885579
 ; GENERAL INFORMATION:
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Damle, Nitin K.
 ; APPLICANT: Brady, William
 ; APPLICANT: Kiener, Peter A.
 ; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 11150 Santa Monica Blvd., Suite 400
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/889,666
 FILING DATE: 08-JUL-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/375390
 FILING DATE: 18-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436-35US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 234 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-889-666-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
 Best Local Similarity 94.0%; Pred. No. 1.4e-105;
 Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;
 QY 1 MACLGFORHKAQLNATRTWPTCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
 Db 1 MACLGFORHKAQLNATRTWPTCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
 QY 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMGNETLFLDSDSXXICTGSSGNQVNLTIQ 118
 Db 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMGNETLFLDSDSXXICTGSSGNQVNLTIQ 120
 QY 119 LRAMDTGLYICKVELMPPPPYL-GINGAQIYVIDPEPC-----PDSDFLLWILAASS 172
 Db 121 LRAMDTGLYICKVELMPPPPYLXGIGNGTQIYVIDPEPCXXXXPDSDFLLWILAASS 180

QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTTGVYVKMPPTPECE--KQFPYFIPIN 223
 Db 181 GLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKMPPTPECEXXXKQFPYFIPIN 234

RESULT 5

US-08-465-078-21
 ; Sequence 21, Application US/08465078
 ; Patent No. 5885796
 ; GENERAL INFORMATION:
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Damle, Nitin K.
 ; APPLICANT: Brady, William
 ; APPLICANT: Kiener, Peter A.
 ; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 11150 Santa Monica Blvd., Suite 400
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,078
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/375390
 FILING DATE: 18-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436-35US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 234 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-465-078-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
 Best Local Similarity 94.0%; Pred. No. 1.4e-105;
 Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;
 QY 1 MACLGFORHKAQLNATRTWPTCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
 Db 1 MACLGFORHKAQLNATRTWPTCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
 QY 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMGNETLFLDSDSXXICTGSSGNQVNLTIQ 118
 Db 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMGNETLFLDSDSXXICTGSSGNQVNLTIQ 120
 QY 119 LRAMDTGLYICKVELMPPPPYL-GINGAQIYVIDPEPC-----PDSDFLLWILAASS 172
 Db 121 LRAMDTGLYICKVELMPPPPYLXGIGNGTQIYVIDPEPCXXXXPDSDFLLWILAASS 180
 QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTTGVYVKMPPTPECE--KQFPYFIPIN 223
 Db 181 GLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKMPPTPECEXXXKQFPYFIPIN 234

us-09-772-103-2.ra1

Mon Jul 1 16:28:06 2002

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; Sequence 21, Application US/08488062
; Patent No. 5977318
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,062
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-062-21

Query Match      94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 1.4e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQLNLAATRTWPCITLLFFLLFIPVFCCKAMHVAQPAVVLAASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNLAARTWPCITLLFFLLFIPVFCCKAMHVAQPAVVLAASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSQVTEVCAATYMGNELTFLDSDS--ICTGTSSGNQVNLTIQG 118
Db 61 ASPGKATEVRVTVLRQADSQVTEVCAATYMGNELTFLDSDSXXICTGTSSGNQVNLTIQG 120
QY 119 LRAMDGTGLYICKVELMYPPIYL-GTNGAQIYVIDPEPC-----PDSDFLLWILAAYSS 172
Db 121 LRAMDGTGLYICKVELMYPPIYLXGIGNGTQIYVIDPEPCXXXXPDSDFLLWILAAYSS 180
QY 173 GLFFYSFLLT-AVSLSKMLKRSPLTTGVVVKMPPTPEPE--KQFPYFIPIN 223
Db 181 GLFFYSFLLTAVSLSKMLKRSPLTTGVVVKMPPTPEPECEXXKQFPYFIPIN 234

RESULT 8
US-08-067-684-14
; Sequence 14, Application US/08067684
; Patent No. 5434131
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.

```


PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-889-666-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLROADSQVTEVCAATYMMGNELT 96
Db 1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLROADSQVTEVCAATYMMGNELT 60

Qy 97 FLDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPPYVLGIGNGAQIYVIDPEP 156
Db 61 FLDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPPYVLGIGNGAQIYVIDPEP 120

Qy 157 CPDSDFLWLILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKKMPPEPECEKQFQ 216
Db 121 CPDSDFLWLILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKKMPPEPECEKQFQ 180

Qy 217 PYFIPIN 223
Db 181 PYFIPIN 187

RESULT 12
US-08-465-078-14
Sequence 14, Application US/08465078
Patent No. 5885796
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kienert, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,078
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-818-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLROADSQVTEVCAATYMMGNELT 96
Db 1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLROADSQVTEVCAATYMMGNELT 60

Qy 97 FLDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPPYVLGIGNGAQIYVIDPEP 156
Db 61 FLDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPPYVLGIGNGAQIYVIDPEP 120

Qy 157 CPDSDFLWLILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKKMPPEPECEKQFQ 216
Db 121 CPDSDFLWLILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKKMPPEPECEKQFQ 180

Qy 217 PYFIPIN 223
Db 181 PYFIPIN 187

RESULT 11
US-08-889-666-14
Sequence 14, Application US/08889666
Patent No. 5885796
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kienert, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,666
FILING DATE: 08-JUL-1997
CLASSIFICATION: 435

NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-078-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCAATYMMGNELT 96
1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCAATYMMGNELT 60
97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMTPPPYVYLGNGAQIYVIDPEP 156
61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMTPPPYVYLGNGAQIYVIDPEP 120
97 CPDSDFLWLLAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVVYKMPPTPECEKQFQ 216
121 CPDSDFLWLLAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVVYKMPPTPECEKQFQ 180
217 PYFIPIN 223
181 PYFIPIN 187

RESULT 13
US-08-725-776-14
Sequence 14, Application US/08725776
Patent No. 5968510

GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELEPHONE: 310-445-1140

TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-725-776-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCAATYMMGNELT 96
1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCAATYMMGNELT 60
97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMTPPPYVYLGNGAQIYVIDPEP 156
61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMTPPPYVYLGNGAQIYVIDPEP 120
97 CPDSDFLWLLAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVVYKMPPTPECEKQFQ 216
121 CPDSDFLWLLAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVVYKMPPTPECEKQFQ 180
217 PYFIPIN 223
181 PYFIPIN 187

RESULT 14
US-08-488-062-14
Sequence 14, Application US/08488062
Patent No. 5977318
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,062
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid

MOLECULE TYPE: protein
US-08-228-208A-14

Query Match 82.6%; Score 970; DB 3; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.le-92; Indels 0; Gaps 0;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIA SFVCEYASPGKATEVRVTVLROADSQVTEVCAATYMMGNELT 96
|||||
Db 1 AMHVAQPAVVLASSRGIA SFVCEYASPGKATEVRVTVLROADSQVTEVCAATYMMGNELT 60
|||||

QY 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMYPYPYLGIGNGAQIYVIDPEP 156
|||||
Db 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMYPYPYLGIGNGAQIYVIDPEP 120
|||||

QY 157 CPDSDFLWLTLAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVVYKMPPTPECEKQFQ 216
|||||
Db 121 CPDSDFLWLTLAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVVYKMPPTPECEKQFQ 180
|||||

QY 217 PYFIPIN 223
|||||
Db 181 PYFIPIN 187
|||||

Search completed: May 7, 2002, 12:01:21
Job time: 149 sec

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-062-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.le-92; Indels 0; Gaps 0;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIA SFVCEYASPGKATEVRVTVLROADSQVTEVCAATYMMGNELT 96
|||||
Db 1 AMHVAQPAVVLASSRGIA SFVCEYASPGKATEVRVTVLROADSQVTEVCAATYMMGNELT 60
|||||

QY 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMYPYPYLGIGNGAQIYVIDPEP 156
|||||
Db 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMYPYPYLGIGNGAQIYVIDPEP 120
|||||

QY 157 CPDSDFLWLTLAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVVYKMPPTPECEKQFQ 216
|||||
Db 121 CPDSDFLWLTLAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVVYKMPPTPECEKQFQ 180
|||||

QY 217 PYFIPIN 223
|||||
Db 181 PYFIPIN 187
|||||

RESULT 15
US-08-228-208A-14
Sequence 14, Application US/08228208A
Patent No. 6090914
GENERAL INFORMATION:
APPLICANT: Liosley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Wallace, Philip M.
TITLE OF INVENTION: CTLA4/CD28lg HYBRID FUSION
TITLE OF INVENTION: PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,208A
FILING DATE: 15-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/008,898
FILING DATE: 22-JAN-1993
APPLICATION NUMBER: 07/723,617
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-30US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310 445-1140
TELEFAX: 310 445-9031
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 11:59:17 ; Search time 32.09 Seconds
(without alignments)
529.353 Million cell updates/sec

Title: US-09-772-103-2
Perfect score: 1174
Sequence: 1 MACLGFORHKAQLNLATRTW.....MPPTPECEKQFPYFIPIN 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

al number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1159	98.7	223	T09536	cytotoxic T-lympho
2	997	84.9	223	T46696	CTLA-4 precursor -
3	970	82.6	186	S08614	cytotoxic T-lympho
4	878	74.8	223	A29063	cytotoxic T-lympho
5	211	18.0	221	S25168	CD28 protein - ch
6	204	17.4	221	T46689	CD28 precursor - r
7	200	17.0	36	T84732	cytotoxic T-lympho
8	187	15.9	220	RWHU28	T-cell surface gly
9	174.5	14.9	173	T46197	cell surface prote
10	170	14.5	218	A43523	T-cell surface gly
11	158	13.5	218	S24413	T-cell surface gly
12	101	8.6	132	S38646	Ig kappa chain V r
13	100.5	8.6	120	S46370	Ig kappa chain V-J
14	99	8.4	124	S40336	Ig kappa chain V-J
15	97	8.3	108	S30521	Ig kappa chain V-J
16	97	8.3	128	S46372	Ig kappa chain var
17	94	8.0	117	S46371	Ig kappa chain V r
18	93	7.9	132	S40334	Ig kappa chain V-J
19	92	7.8	117	S41812	Ig kappa chain - h
20	91	7.8	108	S34007	Ig kappa chain V r
21	91	7.8	4391	A38096	Ig kappa chain V r
22	90.5	7.7	108	S36277	perlecan precursor
23	90.5	7.7	123	S40378	Ig lambda chain V
24	90	7.7	140	PL0013	Ig kappa chain - h
25	89.5	7.6	3707	S18252	Ig kappa chain pre
26	89	7.6	125	S40353	heparan sulfate pr
27	88	7.5	573	S12838	Ig kappa chain V-J
28	87.5	7.5	88	S34104	Ig mu chain precur
29	87.5	7.5	213	A21177	Ig kappa chain V r
					Ig light chain pre

30	87	7.4	207	2	I50609	T-cell surface gly
31	87	7.4	739	2	J50675	vascular cell adhe
32	86	7.3	120	2	S30525	Ig lambda chain V
33	86	7.3	125	2	S40349	Ig kappa chain V-J
34	86	7.3	199	2	S78540	inducible T-cell c
35	86	7.3	234	2	S14237	Ig kappa chain pre
36	86	7.3	739	2	JN0581	vascular cell adhe
37	85.5	7.3	598	2	T42070	protein serine/thr
38	85	7.2	111	2	S36281	Ig lambda chain V
39	85	7.2	112	2	PL0274	Ig kappa chain V r
40	85	7.2	125	2	S40333	Ig kappa chain V-J
41	85	7.2	1367	2	A41228	protein-tyrosine k
42	84.5	7.2	105	2	S26338	Ig kappa chain V r
43	84.5	7.2	124	2	S40318	Ig kappa chain V r
44	84	7.2	111	2	S38497	Ig lambda chain -
45	84	7.2	112	2	H26317	Ig kappa chain V r

ALIGNMENTS

RESULT 1

T09536

cytotoxic T-lymphocyte protein 4 - human

C:Species: Homo sapiens (man)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T09536

R:Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.

J. Immunol. 147, 1037-1044, 1991

A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m

A:Reference number: I49584; MOID:91318145

A:Accession: T09536

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-223 <HAR>

A:Cross-references: EMBL:L15006; NID:g291928; PIDN:AAB59385.1; PID:g291929

C:Genetics:

A:Gene: CTLA4

A:Map position: 2q33

C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

C:Keywords: T-cell; transmembrane protein

Query Match 98.7%; Score 1159; DB 2; Length 223;
Best Local Similarity 98.7%; Pred. No. 4.6e-100;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MACLGFORHKAQLNLATRTWPTCTLLFFLIPVFCAMHVAQPAVYVLASSRGIAFVCEY 60

Db 1 MACLGFORHKAQLNLATRTWPTCTLLFFLIPVFCAMHVAQPAVYVLASSRGIAFVCEY 60

Qy 61 ASPGKATEVRYTVLRQADSOVTEVCAATYMMGNELTFDDSDICTGTSSGNQVNLTIQGLR 120

Db 61 ASPGKATEVRYTVLRQADSOVTEVCAATYMMGNELTFDDSDICTGTSSGNQVNLTIQGLR 120

Qy 121 AMDTGLYICKVELMYPPIYIGNGAQIYVIDPECPDSDFLWLILAAVSSGLFFYSFL 180

Db 121 AMDTGLYICKVELMYPPIYIGNGAQIYVIDPECPDSDFLWLILAAVSSGLFFYSFL 180

Qy 181 LTAVSLSKMLKKRPLTGTGVYVKMPPTPECEKQFPYFIPIN 223

Db 181 LTAVSLSKMLKKRPLTGTGVYVKMPPTPECEKQFPYFIPIN 223

RESULT 2

I46696

CTLA-4 precursor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999

C:Accession: I46696

R:Isono, T.; Seto, A.

Immunogenetics 42, 217-220, 1995

A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole

A:Reference number: I46689; MUID:95369849
A:Accession: I46696
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-223 <LSO>
A:Cross-references: GB:D49844; NID:g755100; PIDN:BA008644.1; PID:g755101
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

Query Match 84.9%; Score 997; DB 2; Length 223;
Best Local Similarity 84.3%; Pred. No. 4.7e-85;
Matches 188; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 MACIGFORHKAQLNLAIRTPWPCILLFELFIPYFCAMHVAQPAVVLASSRGIASEFVCEY 60
DB 1 MARLGFORQGTQLDASRTWSCAALSLFLPVSFKAHVSQPAVVLASSRGVASFVCEY 60
QY 61 ASPCKATEVRVTVLRQADSQVTECAATYAMGNELTFLDDSICTGTSSGNQVNLTIQGLR 120
DB 61 ASSHKATEVRVTVLRQANSQNTVECAATYVENEFLTIDDTCTGISHGNKVNLTIQGLS 120
QY 121 AMDTGLYICKVELMYPYPYILGIGNGAQIYVIDPECPDSEFLWILAAVSSGLFVFSFL 180
DB 121 AMDTGLYICKVELMYPYPYVYVGMGNGTQIVIEPECPDSEFLWILAAVSSGLFVFSFL 180
QY 181 LTAVSLSKMLKKRSPLTGTGVVVKMPPTPECEKQFQYFIPIN 223
DB 181 ITAVSLSKMLKKRSPLTGTGVVVKMPPTPECEKQFQYFIPIN 223

RESULT 3
S08614
cytotoxic T-lymphocyte protein 4 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
C:Accession: S08614
R:Dariaavach, P.; Mattei, M.G.; Golstein, P.; Lefranc, M.P.
Eur. J. Immunol. 18, 1901-1905, 1988
A:Title: Human Ig superfamily CTLA-4 gene: chromosomal localization and identity of prod
A:Reference number: S08614; MUID:89120925
A:Accession: S08614
A:Molecule type: DNA
A:Residues: 1-186 <DAR>
A:Cross-references: EMBL:X15070; NID:g30283; PID:g825649
C:Genetics:
A:Gene: GDB:CTLA4
Map position: 2q33-2q33
Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: transmembrane protein
F:125-150/Domain: transmembrane #status predicted <TMM>
F:151-186/Domain: intracellular #status predicted <INT>
F:21-92/Disulfide bonds: #status predicted

Query Match 82.6%; Score 970; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.2e-82;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 MHVAQPAVVLASSRGIASEFVCEYASPGKATEVRVTVLRQADSQVTECAATYMMGNELTF 97
DB 1 MHVAQPAVVLASSRGIASEFVCEYASPGKATEVRVTVLRQADSQVTECAATYMMGNELTF 97
QY 98 LDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYILGIGNGAQIYVIDPECP 157
DB 61 LDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYILGIGNGAQIYVIDPECP 120
QY 158 PSDFLLWILAAVSSGLFVFSFLTAVSLSKMLKKRSPLTGTGVVVKMPPTPECEKQFQ 217
DB 121 PSDFLLWILAAVSSGLFVFSFLTAVSLSKMLKKRSPLTGTGVVVKMPPTPECEKQFQ 180

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:01:22 ; Search time 19.81 Seconds
(without alignments)
412.734 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGFORHKAQLNLRW.....MPTEPCCKQFQPIPIPIN 223

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	223	1	CTLA_HUMAN
2	1010	86.0	223	1	CTLA_PIG
3	997	84.9	223	1	CTLA_RABIT
4	878	74.8	223	1	CTLA_MOUSE
5	211	18.0	221	1	CD28_CHICK
6	204	17.4	221	1	CD28_RABIT
7	203	17.3	221	1	CD28_BOVIN
8	187	15.9	220	1	CD28_HUMAN
9	170	14.5	218	1	CD28_MOUSE
10	156	13.3	218	1	CD28_RAT
11	91	7.8	4393	1	PGBM_HUMAN
12	89.5	7.6	3707	1	PGBM_MOUSE
13	87	7.4	739	1	VCAI_RAT
14	86	7.3	739	1	VCAI_MOUSE
15	85	7.2	1356	1	VGR2_HUMAN
16	85	7.2	1367	1	VGR2_MOUSE
17	83	7.1	111	1	LV2A_HUMAN
18	83	7.1	111	1	LV2D_HUMAN
19	83	7.1	1343	1	VGR2_RAT
20	82	7.0	215	1	CTB2_HUMAN
21	81.5	6.9	111	1	KV12_RABIT
22	81.5	6.9	1897	1	PTF_HUMAN
23	81	6.9	246	1	MOG_MOUSE
24	79.5	6.8	108	1	KV6K_MOUSE
25	79	6.7	550	1	VGLE_HSVEL
26	78.5	6.7	108	1	KV1H_HUMAN
27	78.5	6.7	108	1	OPCM_RAT
28	78.5	6.7	345	1	OPCM_BOVIN
29	78	6.6	485	1	SAHH_MESCR
30	78	6.6	3038	1	TRIO_HUMAN
31	77.5	6.6	226	1	C79A_HUMAN
32	77.5	6.6	345	1	OPCM_BOVIN
33	77.5	6.6	345	1	OPCM_HUMAN

34	77	6.6	109	1	KV01_RAT
35	76.5	6.5	129	1	KV3M_HUMAN
36	76.5	6.5	1203	1	PTC2_HUMAN
37	76	6.5	109	1	LV2E_HUMAN
38	76	6.5	114	1	KV4A_HUMAN
39	76	6.5	3562	1	PGCV_CHICK
40	75.5	6.4	108	1	KVIG_HUMAN
41	75.5	6.4	149	1	KV5A_MOUSE
42	75.5	6.4	485	1	SAHH_WHEAT
43	75	6.4	112	1	KV2D_MOUSE
44	75	6.4	115	1	KV3I_HUMAN
45	75	6.4	117	1	KV1J_HUMAN

P01681	rattus norv
P18136	homo sapien
O99605	homo sapien
P01708	homo sapien
P01625	homo sapien
Q90953	gallus gall
P01599	homo sapien
P01633	mus musculus
P32112	trititum ae
P01629	mus musculus
P04433	homo sapien
P01602	homo sapien

ALIGNMENTS

RESULT 1	CTLA_HUMAN	STANDARD;	PRT;	223 AA.
ID	CTLA_HUMAN			
AC	P16410;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	CYTOTOXIC T-LYMPHOCYTE PROTEIN 4 PRECURSOR (CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED ANTIGEN 4) (CTLA-4) (CD152 ANTIGEN).			
GN	CTLA4 OR CD152.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	[1]			
RP	SEQUENCE OF 1-37 FROM N.A.			
RX	MEDLINE=91318145; PubMed=1713603;			
RA	Harper K., Balzano C., Rouvier E., Mattei M.-G., Luciani M.F.,			
RA	Golstein P.;			
RT	"CTLA-4 and CD28 activated lymphocyte molecules are closely related			
RT	in both mouse and human as to sequence, message expression, gene			
RT	structure, and chromosomal location.";			
RL	J. Immunol. 147:1037-1044(1991).			
RN	[2]			
RP	SEQUENCE OF 38-223 FROM N.A.			
RC	TISSUE=Lymphocytes;			
RX	MEDLINE=89120925; PubMed=3220103;			
RA	Darlavach P., Mattei M.-G., Golstein P., Lefranc M.-P.;			
RT	"Human Ig superfamily CTLA-4 gene: chromosomal localization and			
RT	identity of protein sequence between murine and human CTLA-4			
RT	cytoplasmic domains.";			
RL	Eur. J. Immunol. 18:1901-1905(1988).			
RN	[3]			
RP	FUNCTION.			
RX	MEDLINE=91341416; PubMed=1714933;			
RA	Linsley P.S., Brady W., Unes M., Grosmaire L.S., Damle N.K.,			
RA	Ledbetter J.A.;			
RT	"CTLA-4 is a second receptor for the B cell activation antigen B7.";			
RL	J. Exp. Med. 174:561-569(1991).			
RN	[4]			
RP	STRUCTURE BY NMR OF 37-165			
RX	MEDLINE=97372889; PubMed=9228944;			
RA	Metzler W.J., Bajorath J., Fenderson W., Shaw S.Y., Constantine K.L.,			
RA	Naemura J., Leytze G., Peach R.J., Lavoie T.B., Mueller L.,			
RA	Linsley P.S.;			
RT	"Solution structure of human CTLA-4 and delineation of a CD80/CD86			
RT	binding site conserved in CD28.";			
RL	Nat. Struct. Biol. 4:527-531(1997).			
CC	-I- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1			
CC	(CD80) AND B7-2 (CD86).			
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-I- TISSUE SPECIFICITY: CELL SURFACE OF ACTIVATED T-LYMPHOCYTES.			
CC	-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.			
CC	-I- DATABASE: NAME=PROW; NOTE=CD guide CD152 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd152.htm".			

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(CD80) AND B7-2 (CD86) (BY SIMILARITY).
 CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC 1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

EMBL; M74363; AAA52127.1; -
 DR EMBL; M37245; AAA52773.1; -
 DR EMBL; M37243; AAA52773.1; JOINED.
 DR EMBL; M37244; AAA52773.1; JOINED.
 DR PIR; S08614; S08614.
 DR PDB; 1AH1; 15-APR-98.
 DR MIM; 123890; -
 DR InterPro: IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal;
 KW 3D-structure.
 KQ SIGNAL 1 35 POTENTIAL.
 FT CHAIN 36 223 CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.
 FT DOMAIN 36 161 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 162 187 POTENTIAL.
 FT DOMAIN 188 223 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 140 IG-LIKE V-TYPE DOMAIN.
 FT DISULFID 58 129 BY SIMILARITY.
 FT DISULFID 85 103 BY SIMILARITY.
 FT CARBOHYD 113 103 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 223 AA; 24626 MW; 7525D6FB3E029B4A CRC64;

Query Match 100.0%; Score 1174; DB 1; Length 223;
 Best Local Similarity 100.0%; Pred. No. 8.9e-102; Indels 0; Gaps 0;
 Matches 223; Conservative 0; Mismatches 0;
 QY 1 MACLGFORHKAQLNLTATWPCITLLFFLLFPVFCCKAMHVAQPAVVLASSRGIAFVCEY 60
 DB 1 MACLGFORHKAQLNLTATWPCITLLFFLLFPVFCCKAMHVAQPAVVLASSRGIAFVCEY 60
 QY 61 ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSGNOVNLTIOGLR 120
 DB 61 ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSGNOVNLTIOGLR 120
 QY 121 AMDTGLYCKVELMPPPPYLYGIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
 DB 121 AMDTGLYCKVELMPPPPYLYGIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
 QY 181 LTAVSLSKMLKKRSPLTTGVYVVKMPPTPECEKQFQYFIPIN 223
 DB 181 LTAVSLSKMLKKRSPLTTGVYVVKMPPTPECEKQFQYFIPIN 223

RESULT 2
 ID CTL4_PIG STANDARD; PRT; 223 AA.
 AC Q9MYX7;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CYTOTOXIC T-LYMPHOCYTE PROTEIN 4 PRECURSOR (CYTOTOXIC T-LYMPHOCYTE-
 DE ASSOCIATED ANTIGEN 4) (CTLA-4).
 GN CTLA4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tachdjian M., Chaplin P.J., Scheerlinck J.-P.Y., Tennent J.M.;
 RT "Molecular characterization and phylogenetic analysis of porcine
 RT cytotoxic T-lymphocyte-associated antigen 4 (CTLA4).";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC 1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1

Query Match 86.0%; Score 1010; DB 1; Length 223;
 Best Local Similarity 85.2%; Pred. No. 1.4e-86;
 Matches 190; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
 QY 1 MACLGFORHKAQLNLTATWPCITLLFFLLFPVFCCKAMHVAQPAVVLASSRGIAFVCEY 60
 DB 1 MACSGFQSHGAWLELTSRTWPCITLLFFLLFPVFCCKAMHVAQPAVVLASSRGIAFVCEY 60
 QY 61 ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSGNOVNLTIOGLR 120
 DB 61 GSAGKAAEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSTENKVNLTIOGLR 120
 QY 121 AMDTGLYCKVELMPPPPYLYGIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
 DB 121 AVDTGLYCKVELLYPPPYVVGNGTQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
 QY 181 LTAVSLSKMLKKRSPLTTGVYVVKMPPTPECEKQFQYFIPIN 223
 DB 181 ITAVSLSKMLKKRSPLTTGVYVVKMPPTPECEKQFQYFIPIN 223

RESULT 3
 ID CTL4_RABIT STANDARD; PRT; 223 AA.
 AC P42072;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CYTOTOXIC T-LYMPHOCYTE PROTEIN 4 PRECURSOR (CYTOTOXIC T-LYMPHOCYTE-
 DE ASSOCIATED ANTIGEN 4) (CTLA-4).
 GN CTLA4.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=B/J X CHBB:HM;
 RA MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules.";
 RT

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:00:52 ; Search time 54.19 Seconds
(without alignments)
601.933 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGQRHKAQLNLAIRTW.....MPTEPCERKQFYFIPIN 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1122	95.6	223	6 Q9BDN7	Q9bdn7 papio anubi
2	1118	95.2	223	6 Q9BDC4	Q9bdc4 macaca mulla
3	1076	91.7	223	6 Q9BDP1	Q9bdp1 aotus trivi
4	1034	88.1	223	6 Q9XTA1	Q9xta1 felis silve
5	1032	87.9	223	6 Q9FT02	Q9ft02 canis famil
6	1022	87.1	223	6 Q9GKP2	Q9gkp2 canis famil
7	1014	86.4	223	6 Q9XSY7	Q9xsy7 felis silve
8	1006	85.7	223	6 Q9N186	Q9n186 sus scrofa
9	997	84.9	223	6 Q9XS11	Q9xs11 canis famil
10	996	84.8	223	11 Q9JLV3	Q9jlv3 marmota mon
11	984	83.8	221	6 Q28090	Q28090 bos taurus
12	975	83.0	221	6 Q97631	Q97631 ovis aries
13	896	76.3	223	11 Q62859	Q62859 rattus norv
14	882	75.1	223	11 Q9QZ27	Q9qzz2 mus musculu
15	592	50.4	137	4 Q95653	Q95653 homo sapien
16	587	50.0	115	4 Q9BZK2	Q9bz2k homo sapien
17	534	45.5	174	11 Q9Z1A7	Q9z1a7 rattus norv
18	442	37.6	84	4 Q9UKN9	Q9ukn9 homo sapien
19	252	21.5	68	11 Q99PF8	Q99pf8 cricetus

20	199.5	17.0	221	6 Q9GKP3	Q9gkp3 canis famil
21	198	16.9	219	6 Q97630	Q97630 ovis aries
22	196.5	16.7	221	6 Q9N0N8	Q9n0n8 canis famil
23	191.5	16.3	221	6 Q02757	Q02757 felis silve
24	190.5	16.2	221	6 Q9N214	Q9n214 felis silve
25	189	16.1	220	6 Q9BDN2	Q9bdn2 callithrix
26	188.5	16.1	220	6 Q9BDN8	Q9bdn8 papio anubi
27	187.5	16.0	220	6 Q9BDM8	Q9bdm8 macaca neme
28	186.5	15.9	220	6 Q9BDN5	Q9bdn5 cercocobus
29	185.5	15.8	221	11 Q9JLV4	Q9jlv4 marmota mon
30	178.5	15.2	220	6 Q9BDM6	Q9bdm6 macaca mulla
31	174.5	14.9	173	6 Q28289	Q28289 canis famil
32	113.5	9.7	201	4 Q14931	Q14931 homo sapien
33	110	9.4	176	4 Q95667	Q95667 homo sapien
34	108	9.2	44	11 Q9Z1A8	Q9z1a8 mus musculu
35	107	9.1	177	4 Q14930	Q14930 homo sapien
36	103.5	8.8	152	4 Q95668	Q14932 homo sapien
37	103.5	8.8	165	4 Q95669	Q95668 homo sapien
38	97	8.3	269	4 Q95297	Q95669 homo sapien
39	96	8.2	108	4 Q9UL79	Q95297 homo sapien
40	94.5	8.0	243	4 Q9UELA	Q9ul79 homo sapien
41	94	8.0	209	4 Q9NYK4	Q9uel4 homo sapien
42	91.5	7.8	183	4 Q9UEL6	Q9nyk4 homo sapien
43	91.5	7.8	183	4 Q9UEL6	Q9uel6 homo sapien
44	91.5	7.8	235	11 Q99M11	Q99m11 mus musculu
45	91	7.8	4370	4 Q9H3V5	Q9h3v5 homo sapien

ALIGNMENTS

RESULT 1

Q9BDN7 PRELIMINARY; PRT; 223 AA.
ID Q9BDN7
AC Q9BDN7
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CDI52 PROTEIN PRECURSOR.
GN CTLA-4.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Papio.
OX NCBI_Taxid=9555;
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL; AF344838; AAK37534.1; -.
KW Signal.
FT SIGNAL
SQ SEQUENCE 223 AA; 24655 MW; EC18C279CCCC5668 CRC64;

Query Match 95.6%; Score 1122; DB 6; Length 223;
Best Local Similarity 96.9%; Pred. No. 4.6e-99;
Matches 216; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY	1	MACLGQRHKAQLNLAIRTWPCITLLFELLPVCKAMHVAQPAVVLASRGTSFVCEY	60
Db	1	MACLGQRHKAQLNLAIRTPYLLSFLFIPVFSKAMHVAQPAVVLASRGTSFVCEY	60
QY	61	ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELFLDDSICTGTSGNQVNLTIQGLR	120
Db	61	ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELFLDDSICTGTSGNQVNLTIQGLR	120
QY	121	AMDTGLYICKVELMYPYPPYLLGNGAQIYIDPEPCPSDFLLWLTAAYSSGLFFYSFL	180
Db	121	AMDTGLYICKVELMYPYPPYLLGNGAQIYIDPEPCPSDFLLWLTAAYSSGLFFYSFL	180

QY 181 LTAVALSKMLKKRSPLTGVVYKMPPTPECEKQFQYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTGVVYKMPPTPECEKQFQYFIPIN 223

RESULT 2
Q9BDC4 PRELIMINARY; PRT; 223 AA.
AC Q9BDC4; 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CD152 PROTEIN PRECURSOR.
GN CTLA-4.
OS Macaca mulatta (Rhesus macaque),
OS Macaca nemestrina (pig-tailed macaque), and
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9544, 9545, 9531;
[1]
RN SEQUENCE FROM N.A.
RP SPECIES=M.mulatta, M.nemestrina, and C.torquatus atys;
RC Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RA "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Pas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL; AF344846; AAK37605.1; -.
DR EMBL; AF344854; AAK37537.1; -.
DR EMBL; AF344848; AAK37608.1; -.
KW Signal.
FT SIGNAL 1 37 POTENTIAL.
FT VARIANT 223 223 N -> D.
FT SEQUENCE 223 AA; 24683 MW; BDB42248A00398FA CRC64;

Query Match 95.2%; Score 1118; DB 6; Length 223;
Best Local Similarity 96.4%; Pred. No. 1.le-98;
Matches 215; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MACIGFORHKAQLNLTATRTWPCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACIGFORHKAQLNLTATRTWPCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60

QY 61 ASPGKATEVRVTLRQADSOVTEVCAATYMMGNELTFLDSDICTGSSGNQVNLTIQGLR 120
DB 61 ASPGKATEVRVTLRQADSOVTEVCAATYMMGNELTFLDSDICTGSSGNQVNLTIQGLR 120

QY 121 AMDTGLYICKVELMYPYVYLGNGAQIYVIDPEPCPDSDFLWILAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMYPYVYLGNGAQIYVIDPEPCPDSDFLWILAAVSSGLFFYSFL 180

QY 181 LTAVALSKMLKKRSPLTGVVYKMPPTPECEKQFQYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTGVVYKMPPTPECEKQFQYFIPIN 223

RESULT 3
Q9BDP1 PRELIMINARY; PRT; 223 AA.
AC Q9BDP1; 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CD152 PROTEIN PRECURSOR.
GN CTLA-4.
OS Aotus trivirgatus (Night monkey) (Douroucoulis).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=9505;

[1]
RN SEQUENCE FROM N.A.
RP Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RA "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Pas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL; AF344834; AAK37530.1; -.
KW Signal.
FT SIGNAL 1 37 POTENTIAL.
FT SEQUENCE 223 AA; 24813 MW; 3F702052117C1431 CRC64;

Query Match 91.7%; Score 1076; DB 6; Length 223;
Best Local Similarity 91.5%; Pred. No. 1.le-94;
Matches 204; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 MACIGFORHKAQLNLTATRTWPCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACIGFORHKAQLNLTATRTWPCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60

QY 61 ASPGKATEVRVTLRQADSOVTEVCAATYMMGNELTFLDSDICTGSSGNQVNLTIQGLR 120
DB 61 ASPGKATEVRVTLRQADSOVTEVCAATYMMGNELTFLDSDICTGSSGNQVNLTIQGLR 120

QY 121 AMDTGLYICKVELMYPYVYLGNGAQIYVIDPEPCPDSDFLWILAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMYPYVYLGNGAQIYVIDPEPCPDSDFLWILAAVSSGLFFYSFL 180

QY 181 LTAVALSKMLKKRSPLTGVVYKMPPTPECEKQFQYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTGVVYKMPPTPECEKQFQYFIPIN 223

RESULT 4
Q9XTA1 PRELIMINARY; PRT; 223 AA.
AC Q9XTA1; 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED 4 (COSTIMULATORY MOLECULE B7 RECEPTOR CD152).
GN CTLA4 OR CTLA-4 OR CD152.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
[1]
RN SEQUENCE FROM N.A.
RP Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA Mikami T., Takahashi E.;
RT "Molecular cloning and sequencing of a cDNA encoding the feline
RT cytotoxic T-lymphocyte-associated 4 (CTLA4) homologue.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP Choi I.-S., Hash S., Collisson E.W.;
RA "Sequence analyses of the feline CD28 and CTLA-4.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP Yang S., Sim G.-K.;
RT "Nucleotide and Predicted Amino Acid Sequences of Canine and Feline
RT CD152 (CTLA4).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AB029395; BAA82273.1; -.
DR EMBL; AF170725; AAD50988.1; -.
DR EMBL; AF154844; AAG43372.1; -.
DR HSP; P16410; IAH1.
DR InterPro; IPR003599; Ig.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 11:58:42 ; Search time 53.91 seconds
(without alignments)
306.406 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGQRHKAQLNLRTRW.....MPTEPECEKQFPYFIPIN 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

al number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*

1:	/SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2:	/SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3:	/SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4:	/SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5:	/SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6:	/SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7:	/SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8:	/SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9:	/SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10:	/SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11:	/SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12:	/SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13:	/SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14:	/SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15:	/SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16:	/SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17:	/SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18:	/SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19:	/SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20:	/SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21:	/SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22:	/SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1174	100.0	223	22	Human CTLA4.
2	1170	99.7	223	21	Human CTLA-4 prote
3	1159	98.7	223	18	Soluble human CTLA
4	1159	98.7	223	22	Human CTLA4 protei
5	1103.5	94.0	234	20	Human CTLA4 protei
6	1034	88.1	223	20	Feline CTLA4 prote
7	1022	87.1	223	20	Canine CTLA4 prote
8	1015	86.5	223	21	Feline CTLA-4. Fe
9	1015	86.5	223	21	Cat CTLA-4 recepto
10	1006	85.7	223	21	Porcine CTLA-4 sol
11	984.5	83.9	211	20	Human CTLA4 recept

12	983	83.7	212	15	AAR60134	CTLA4 receptor fus
13	983	83.7	212	16	AAR77642	Full length CTLA4
14	983	83.7	212	20	AAW43479	Amino acid sequenc
15	983	83.7	212	20	AAW81584	Human CTLA4 recept
16	979	83.4	212	14	AAR31040	Human CTLA4 recept
17	977	83.2	223	22	AAU00686	Porcine CTLA4 prot
18	970	82.6	187	20	AAU41130	CTLA4 receptor wit
19	970	82.6	187	20	AAW97615	Human CTLA recepto
20	970	82.6	187	20	AAW97610	Human CTLA recepto
21	967	82.4	187	17	AAW86945	Human T cell speci
22	957	81.5	187	19	AAW29728	Soluble CTLA4 muta
23	837	71.3	168	19	AAW42340	CTLA-4 extracellul
24	804.5	68.5	234	20	AAU41134	Mouse CTLA4 protei
25	686	58.4	400	21	AAU15123	Porcine CTLA-4-Ig
26	672	57.2	364	21	AAU93698	Fusion protein of
27	667.5	56.9	377	18	AAW26208	CTLA4-modified IgG
28	667	56.8	374	18	AAW26206	CTLA4-IgG4 fusion
29	667	56.8	374	18	AAW26207	CTLA4-modified IgG
30	658	56.0	260	22	AAU00685	Human CTLA4-human
31	648	55.2	124	18	AAW35847	Human CTLA4 for us
32	648	55.2	357	18	AAW35863	Human CTLA4:IgG2a
33	642	54.7	357	19	AAW68134	Amino acid sequenc
34	642	54.7	470	19	AAW68135	Amino acid sequenc
35	638.5	54.4	253	20	AAU41132	CTLA4/E7 fusion pr
36	638.5	54.4	253	20	AAU43480	Amino acid sequenc
37	638.5	54.4	253	20	AAU01502	Amino terminal CTL
38	638.5	54.4	253	20	AAW97612	Amino terminal CTL
39	638.5	54.4	253	20	AAW81586	CTLA4-E7 fusion pr
40	638.5	54.4	253	20	AAW81586	CTLA4/E7 fusion pr
41	638.5	54.4	502	20	AAU41131	CTLA4/p97 fusion p
42	638.5	54.4	502	20	AAU43605	Amino acid sequenc
43	638.5	54.4	502	20	AAW97616	Amino terminal CTL
44	638.5	54.4	502	20	AAW97611	Amino terminal CTL
45	638.5	54.4	502	20	AAW87561	CTLA4-p97 fusion p

ALIGNMENTS

RESULT 1

AGS66519
ID AAG66519 standard; Protein; 223 AA.

XX AAG66519;

DT 22-OCT-2001 (first entry)

XX Human CTLA4.

XX Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;

KW Immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;

KW T cell; humanised antibody; autoimmune disorder; graft rejection;

KW allergy.

XX Homo sapiens.

XX WO200154732-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US02653.

XX 27-JAN-2000; 2000US-0178473.

XX (GEMY) GENETICS INST INC.

XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;

XX O'Hara D, Hinton P, Tsurushita N;

XX WPI; 2001-483195/52.

XX N-PSDB; AAH76437.

XX Novel antibody-toxic group conjugate comprising an antibody that

PT recognizes a molecule expressed only on activated T cells, useful for
 PT modulating immune response for treating autoimmune disorder, allergic
 PT response

Example 3; Page 114-115; 123pp; English.

XX The invention relates to an antibody-toxic group conjugate comprising
 XX an antibody that specifically recognises a molecule expressed only on
 XX activated T cells, and a toxic group. The T cell molecule is
 XX preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).
 XX The antibody of the invention is a humanised anti-CTLA4 antibody
 XX comprising a sequence of 128 or 142 amino acids fully defined in the
 XX specification. The antibody-toxic group conjugate is useful for
 XX modulating the immune response in a subject suffering from a disorder
 XX or condition such as autoimmune disorder, immune response to a graft,
 XX allergic response or an immune response to a therapeutic protein.
 XX The antibody is also useful for research purposes, e.g., in staining
 XX and isolating CTLA4-bearing cells. The antibody is also useful for
 XX T-cell typing, for isolating specific IL-2 receptor-bearing cells or
 XX fragments of the receptor, for vaccine preparation, and for determining
 XX the effectiveness of an agent to down-regulate CTLA4 activity. The
 XX present sequence is human CTLA4, which is bound by the antibody
 XX provided in the invention.

XX Sequence 223 AA;

Query Match 100.0%; Score 1174; DB 22; Length 223;
 Best Local Similarity 100.0%; Pred. No. 3e-106;
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACIGFORHKAQLNLTATWPCTLLFFLLFPVCKAMHVAQPAVLASSRGIAFVCEY 60
 DB 1 macigfgrhkaqlnltatwpctllffllfpvckamhvaqpavlassrgiasfvey 60
 QY 61 ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLLDSDICTSGNOVNLTIOGLR 120
 DB 61 aspgkatevrvtvltlrqadsqvtevcattymmgneftfllddictsgnqvnltioglrl 120
 QY 121 AMDTGLYCKVELMYPYPIYIGNGAQIYVIDPEPCDPSDFLLWILAASVSGLFFYSFL 180
 DB 121 amdgtglyckvelmypyypiyigngaqiyvidpepcdpsdflwilaavssgiffysfl 180
 QY 181 LTAVSLSKMLKKRSLPTGTGVYVKMPPTPECEKQFPYFIPIN 223
 DB 181 ltavslskmlkkrslptgtgvvkmppptpecekekqfpyfipin 223

BLT 2

ID 5129
 AC AAV15129 standard; protein; 223 AA.

AC AAV15129;

DT 07-FEB-2000 (first entry)

DE Human CTLA-4 protein.

KW Human CTLA-4; soluble protein; xenograft; organ transplant; B7; CD28;
 KW xenograft-specific immunosuppression; recipient T-cell; anergy;
 KW co-stimulatory signal 2; homology; porcine CTLA-4.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX Peptide 1..37
 XX /label= Signal_peptide

XX W09957266-A2.

XX 11-NOV-1999.

XX 30-APR-1959; 99WO-GB01350.

XX 30-APR-1998; 98GB-0009280.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Lechler IR, Dorling A;

XX WPI; 2000-038815/03.

XX N-PSDB; AAZ29001.

XX Inhibiting T-cell mediated rejection of xenotransplanted organs

XX Disclosure; Fig 15; 43pp; English.

XX The present sequence is the human CTLA-4 soluble protein for
 XX xenograft-specific immunosuppression. Soluble CTLA-4 when administered to
 XX the organ recipient preferentially binds B7 on the xenograft and blocks
 XX its interaction with CD28 on recipient T-cells. The delivery of co
 XX -stimulatory signal 2 is blocked and the T-cells are rendered anergic.
 XX This sequence has an overall homology of 85.2% with porcine CTLA-4 DNA.

XX Sequence 223 AA;

Query Match 99.7%; Score 1170; DB 21; Length 223;
 Best Local Similarity 99.6%; Pred. No. 7.4e-106;
 Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MACIGFORHKAQLNLTATWPCTLLFFLLFPVCKAMHVAQPAVLASSRGIAFVCEY 60
 DB 1 macigfgrhkaqlnltatwpctllffllfpvckamhvaqpavlassrgiasfvey 60
 QY 61 ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLLDSDICTSGNOVNLTIOGLR 120
 DB 61 aspgkatevrvtvltlrqadsqvtevcattymmgneftfllddictsgnqvnltioglrl 120
 QY 121 AMDTGLYCKVELMYPYPIYIGNGAQIYVIDPEPCDPSDFLLWILAASVSGLFFYSFL 180
 DB 121 amdgtglyckvelmypyypiyigngaqiyvidpepcdpsdflwilaavssgiffysfl 180
 QY 181 LTAVSLSKMLKKRSLPTGTGVYVKMPPTPECEKQFPYFIPIN 223
 DB 181 ltavslskmlkkrslptgtgvvkmppptpecekekqfpyfipin 223

RESULT 3

ID AAW25111

AC AAW25111 standard; protein; 223 AA.

AC AAW25111;

DT 03-NOV-1997 (first entry)

DE Soluble human CTLA4 mutant molecule reactive with CD80 antigen.

KW CTLA4; mutant; soluble; CD80 antigen; specific; immune system;
 KW T cell surface receptor; B7-1; antibody production inhibitor; allergy;
 KW autoimmune disease; chronic inflammation; allograft rejection;
 KW graft versus host disease.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX Peptide 1..37
 XX /label= sig_peptide
 XX Protein 38..234
 XX /label= mat_protein
 XX Region 62..67
 XX /note= "CDR 1-like region"
 XX Region 86..90
 XX /note= "CDR 2-like region"
 XX Region 132..139
 XX /note= "CDR 3-like region; highly conserved"